

EAST Search History

| Ref # | Hits | Search Query | DBs | Default Operator | Plurals | Time Stamp |
|-------|------|---|--|------------------|---------|------------------|
| S1 | 2 | WO-9632106-\$.did. | EPO; DERWENT | OR | OFF | 2006/08/09 10:55 |
| S2 | 1 | "4840915".pn. | USPAT | OR | OFF | 2006/08/09 10:56 |
| S3 | 1 | "4486538".pn. | USPAT | OR | OFF | 2006/08/09 10:57 |
| S4 | 1 | "4298590".pn. | USPAT | OR | OFF | 2006/08/09 10:58 |
| S5 | 52 | Bogoch.in. | US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT | OR | OFF | 2006/08/09 10:59 |
| S6 | 12 | aglycoprotein | US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT | OR | ON | 2006/08/09 11:00 |
| S7 | 45 | antimalignin OR (malignin AND antibody) | US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT | OR | ON | 2006/08/09 11:01 |
| S8 | 32 | S5 AND (S6 OR S7) | US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT | OR | ON | 2006/08/09 11:02 |

10/642,587 STN STRATEGY

(FILE 'HOME' ENTERED AT 14:56:35 ON 09 AUG 2006)

FILE 'MEDLINE, BIOSIS, LIFESCI, EMBASE, SCISEARCH, CAPLUS'
ENTERED AT

14:56:59 ON 09 AUG 2006

L1 0 S BOGOCH/AU
L2 5 S BOGOCH
L3 10 S AGLYCOPROTEIN
L4 91 S MALIGNIN
L5 58 DUP REM L4 (33 DUPLICATES REMOVED)
L6 40 S L5 AND ANTIBODY
L7 4 S AGLYCO AND 10B
L8 3 DUP REM L7 (1 DUPLICATE REMOVED)
L9 44 S GLYCOPROTEIN AND 10B
L10 31 DUP REM L9 (13 DUPLICATES REMOVED)

10/642,587 Sequence search
08/09/2006
Public databases

SEQ ID NO: 1

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------|--------------------|
| 1 | 85 | 100.0 | 16 | 3 | AAy87638 | Aay87638 Human bra |
| 2 | 85 | 100.0 | 16 | 5 | ABG94714 | Abg94714 Glioma re |
| 3 | 85 | 100.0 | 16 | 6 | ABU57264 | Abu57264 Replikin |
| 4 | 85 | 100.0 | 16 | 7 | ADD88337 | Add88337 Human mal |
| 5 | 85 | 100.0 | 16 | 7 | ADG18115 | Adg18115 Glioma Re |
| 6 | 85 | 100.0 | 16 | 9 | ADW92264 | Adw92264 Isolated |
| 7 | 64 | 75.3 | 15 | 2 | AAW15757 | Aaw15757 Peptide f |
| 8 | 52 | 61.2 | 10 | 5 | ABG94733 | Abg94733 Glioma re |
| 9 | 52 | 61.2 | 10 | 6 | ABU57283 | Abu57283 Replikin |
| 10 | 52 | 61.2 | 10 | 9 | ADW92283 | Adw92283 Malignin |
| 11 | 51 | 60.0 | 10 | 5 | ABG94711 | Abg94711 Glioma re |
| 12 | 51 | 60.0 | 10 | 5 | ABG94793 | Abg94793 Replikin |
| 13 | 51 | 60.0 | 10 | 6 | ABU57343 | Abu57343 Replikin |
| 14 | 51 | 60.0 | 10 | 6 | ABU57261 | Abu57261 Replikin |
| 15 | 51 | 60.0 | 10 | 7 | ADD88416 | Add88416 Cancer ce |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------------------|-------------------|
| 1 | 85 | 100.0 | 16 | 2 | US-09-146-755-1 | Sequence 1, Appli |
| 2 | 85 | 100.0 | 16 | 2 | US-09-817-144-1 | Sequence 1, Appli |
| 3 | 46 | 54.1 | 717 | 2 | US-09-487-558B-376 | Sequence 376, App |
| 4 | 46 | 54.1 | 738 | 2 | US-09-538-092-575 | Sequence 575, App |
| 5 | 43 | 50.6 | 464 | 2 | US-09-050-739-62 | Sequence 62, Appl |
| 6 | 43 | 50.6 | 464 | 2 | US-09-804-980-62 | Sequence 62, Appl |
| 7 | 43 | 50.6 | 474 | 2 | US-08-311-731A-353 | Sequence 353, App |
| 8 | 42 | 49.4 | 236 | 2 | US-09-270-767-56840 | Sequence 56840, A |
| 9 | 42 | 49.4 | 313 | 2 | US-09-252-991A-31437 | Sequence 31437, A |
| 10 | 40.5 | 47.6 | 465 | 2 | US-10-029-180-44 | Sequence 44, Appl |
| 11 | 40 | 47.1 | 219 | 2 | US-09-107-532A-5590 | Sequence 5590, Ap |
| 12 | 40 | 47.1 | 223 | 2 | US-09-248-796A-24488 | Sequence 24488, A |
| 13 | 39.5 | 46.5 | 477 | 2 | US-10-029-180-54 | Sequence 54, Appl |
| 14 | 39 | 45.9 | 199 | 2 | US-10-101-464A-694 | Sequence 694, App |
| 15 | 39 | 45.9 | 235 | 2 | US-09-252-991A-16701 | Sequence 16701, A |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|-------------------|-------------------|
| 1 | 85 | 100.0 | 16 | 3 | US-09-984-056-4 | Sequence 4, Appli |
| 2 | 85 | 100.0 | 16 | 3 | US-09-984-057-4 | Sequence 4, Appli |
| 3 | 85 | 100.0 | 16 | 3 | US-09-817-144-1 | Sequence 1, Appli |
| 4 | 85 | 100.0 | 16 | 4 | US-10-105-232-4 | Sequence 4, Appli |
| 5 | 85 | 100.0 | 16 | 4 | US-10-189-437-4 | Sequence 4, Appli |
| 6 | 85 | 100.0 | 16 | 4 | US-10-642-587-1 | Sequence 1, Appli |
| 7 | 85 | 100.0 | 16 | 5 | US-10-860-050-4 | Sequence 4, Appli |
| 8 | 74.5 | 87.6 | 17 | 5 | US-10-860-050-866 | Sequence 866, App |
| 9 | 52 | 61.2 | 10 | 5 | US-10-860-050-23 | Sequence 23, Appl |
| 10 | 51 | 60.0 | 10 | 3 | US-09-984-056-1 | Sequence 1, Appli |
| 11 | 51 | 60.0 | 10 | 3 | US-09-984-056-83 | Sequence 83, Appl |
| 12 | 51 | 60.0 | 10 | 3 | US-09-984-057-1 | Sequence 1, Appli |
| 13 | 51 | 60.0 | 10 | 3 | US-09-984-057-83 | Sequence 83, Appl |
| 14 | 51 | 60.0 | 10 | 4 | US-10-105-232-1 | Sequence 1, Appli |
| 15 | 51 | 60.0 | 10 | 4 | US-10-105-232-83 | Sequence 83, Appl |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|-----------------------|-------------------|
| 1 | 44 | 51.8 | 2014 | 7 | US-11-299-791-18 | Sequence 18, Appl |
| 2 | 42 | 49.4 | 50 | 6 | US-10-953-349-36303 | Sequence 36303, A |
| 3 | 42 | 49.4 | 170 | 7 | US-11-056-355B-21194 | Sequence 21194, A |
| 4 | 42 | 49.4 | 170 | 7 | US-11-056-355B-49330 | Sequence 49330, A |
| 5 | 42 | 49.4 | 170 | 7 | US-11-056-355B-105131 | Sequence 105131, |
| 6 | 42 | 49.4 | 170 | 7 | US-11-056-355B-116370 | Sequence 116370, |
| 7 | 42 | 49.4 | 262 | 7 | US-11-056-355B-21193 | Sequence 21193, A |
| 8 | 42 | 49.4 | 262 | 7 | US-11-056-355B-49329 | Sequence 49329, A |
| 9 | 42 | 49.4 | 262 | 7 | US-11-056-355B-105130 | Sequence 105130, |
| 10 | 42 | 49.4 | 262 | 7 | US-11-056-355B-116369 | Sequence 116369, |
| 11 | 41 | 48.2 | 80 | 7 | US-11-056-355B-25462 | Sequence 25462, A |
| 12 | 41 | 48.2 | 80 | 7 | US-11-056-355B-37890 | Sequence 37890, A |
| 13 | 41 | 48.2 | 80 | 7 | US-11-056-355B-42910 | Sequence 42910, A |
| 14 | 41 | 48.2 | 80 | 7 | US-11-056-355B-43439 | Sequence 43439, A |
| 15 | 41 | 48.2 | 97 | 7 | US-11-056-355B-25461 | Sequence 25461, A |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|--------|--------------------|
| 1 | 48 | 56.5 | 468 | 2 | AG2899 | dihydrolipoamide d |
| 2 | 48 | 56.5 | 468 | 2 | H97674 | dihydrolipoamide d |
| 3 | 47 | 55.3 | 532 | 2 | AC3359 | dihydrolipoamide d |
| 4 | 46 | 54.1 | 738 | 1 | S51380 | protein kinase STE |
| 5 | 45 | 52.9 | 280 | 2 | JU0294 | levansucrase gene |
| 6 | 45 | 52.9 | 336 | 2 | D42653 | dihydrolipoamide d |
| 7 | 43 | 50.6 | 321 | 2 | C81746 | peptide ABC transp |
| 8 | 43 | 50.6 | 464 | 2 | B70828 | hypothetical prote |
| 9 | 43 | 50.6 | 467 | 2 | G87207 | dihydrolipoamide d |
| 10 | 43 | 50.6 | 481 | 2 | AB2753 | dihydrolipoamide d |
| 11 | 43 | 50.6 | 481 | 2 | H97533 | dihydrolipoamide d |
| 12 | 42 | 49.4 | 262 | 2 | T52310 | Lil3 protein [impo |
| 13 | 42 | 49.4 | 350 | 2 | G71445 | hypothetical prote |
| 14 | 41 | 48.2 | 105 | 2 | G89993 | hypothetical prote |
| 15 | 41 | 48.2 | 222 | 2 | C89944 | conserved hypothet |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|--------------|--------------------|
| 1 | 48 | 56.5 | 468 | 2 | Q2K3F8_RHIET | Q2k3f8 rhizobium e |
| 2 | 48 | 56.5 | 468 | 2 | Q8UC66_AGRT5 | Q8uc66 agrobacteri |
| 3 | 48 | 56.5 | 468 | 2 | Q98ED5_RHILO | Q98ed5 rhizobium l |
| 4 | 47 | 55.3 | 481 | 2 | Q2K8W2_RHIET | Q2k8w2 rhizobium e |
| 5 | 47 | 55.3 | 486 | 2 | Q6G167_BARQU | Q6g167 bartonella |
| 6 | 47 | 55.3 | 486 | 2 | Q6G402_BARHE | Q6g402 bartonella |
| 7 | 47 | 55.3 | 487 | 2 | Q57D13_BRUAB | Q57d13 brucella ab |
| 8 | 47 | 55.3 | 487 | 2 | Q8G0G9_BRUSU | Q8g0g9 brucella su |
| 9 | 47 | 55.3 | 487 | 2 | Q2YPV6_BRUA2 | Q2ypv6 brucella ab |
| 10 | 47 | 55.3 | 532 | 2 | Q8YHE4_BRUME | Q8yhe4 brucella me |
| 11 | 46 | 54.1 | 187 | 2 | Q9EV54_RHIME | Q9ev54 rhizobium m |
| 12 | 46 | 54.1 | 462 | 2 | Q74HV2_LACJO | Q74hv2 lactobacill |
| 13 | 46 | 54.1 | 467 | 2 | Q5YNX4_NOCFA | Q5ynx4 nocardia fa |
| 14 | 46 | 54.1 | 481 | 2 | Q92Q96_RHIME | Q92q96 rhizobium m |
| 15 | 46 | 54.1 | 481 | 2 | Q98MY4_RHILO | Q98my4 rhizobium l |

NA ENCODING SEQ ID NO: 1

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description |
|------------|-------|-------|--------|----|-------------|--------------------|
| | | Match | Length | | | |
| c 1 | 55 | 64.7 | 218983 | 11 | AC171274 | AC171274 Gallus ga |
| c 2 | 55 | 64.7 | 225652 | 11 | AC169087 | AC169087 Gallus ga |
| c 3 | 53 | 62.4 | 94320 | 5 | AC002564 | AC002564 Homo sapi |
| c 4 | 53 | 62.4 | 152145 | 12 | AC069570 | AC069570 Homo sapi |
| c 5 | 53 | 62.4 | 162023 | 5 | AC147027 | AC147027 Pan trogl |
| c 6 | 53 | 62.4 | 177687 | 12 | AC093321 | AC093321 Homo sapi |
| c 7 | 53 | 62.4 | 187139 | 5 | AC161021 | AC161021 Pan trogl |
| c 8 | 53 | 62.4 | 189756 | 5 | AC161472 | AC161472 Pan trogl |
| c 9 | 52 | 61.2 | 110000 | 15 | CP000250_39 | Continuation (40 o |
| c 10 | 52 | 61.2 | 125713 | 6 | AL670928 | AL670928 Mouse DNA |
| c 11 | 51 | 60.0 | 160299 | 12 | AC150969 | AC150969 Bos tauru |
| c 12 | 51 | 60.0 | 173326 | 12 | AC151220 | AC151220 Bos tauru |
| c 13 | 51 | 60.0 | 217285 | 12 | AC126317 | AC126317 Rattus no |
| c 14 | 51 | 60.0 | 260760 | 12 | AC127861 | AC127861 Rattus no |
| c 15 | 50 | 58.8 | 79355 | 12 | AC021280 | AC021280 Homo sapi |

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description |
|------------|-------|-------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| c 1 | 48 | 56.5 | 1395 | 13 | ADS62510 | Ads62510 Bacterial |
| c 2 | 48 | 56.5 | 1395 | 13 | ADS62902 | Ads62902 Bacterial |
| c 3 | 48 | 56.5 | 1395 | 13 | ADS59449 | Ads59449 Bacterial |
| c 4 | 48 | 56.5 | 1407 | 13 | ADS60067 | Ads60067 Bacterial |
| c 5 | 47.5 | 55.9 | 23603 | 13 | ABD33391 | Abd33391 Murine ca |
| c 6 | 47 | 55.3 | 5233 | 8 | AAD55425 | Aad55425 Human FGF |
| c 7 | 47 | 55.3 | 33352 | 9 | ADA02846 | Ada02846 Human FGF |
| c 8 | 47 | 55.3 | 33352 | 10 | ADB72584 | Adb72584 Human FGF |
| c 9 | 47 | 55.3 | 33352 | 10 | ADC85325 | Adc85325 Mouse Fgf |
| c 10 | 47 | 55.3 | 33352 | 12 | ADM74441 | Adm74441 Human car |
| c 11 | 47 | 55.3 | 35558 | 14 | ADZ12667 | Adz12667 Human can |
| c 12 | 47 | 55.3 | 117754 | 11 | ACN43866 | Acn43866 Human gen |
| c 13 | 47 | 55.3 | 127943 | 12 | ADQ97651 | Adq97651 Human can |
| c 14 | 46 | 54.1 | 793 | 8 | ABZ52278 | Abz52278 Aspergill |
| c 15 | 46 | 54.1 | 1446 | 13 | ADS59836 | Ads59836 Bacterial |

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description |
|------------|-------|-------|--------|----|---------------------|-------------------|
| | | Match | Length | | | |
| c 1 | 47 | 55.3 | 17352 | 3 | US-09-949-016-12990 | Sequence 12990, A |
| c 2 | 47 | 55.3 | 218940 | 3 | US-09-949-016-17539 | Sequence 17539, A |
| c 3 | 46 | 54.1 | 2154 | 3 | US-09-487-558B-375 | Sequence 375, App |
| c 4 | 44 | 51.8 | 348 | 3 | US-09-621-976-12993 | Sequence 12993, A |
| c 5 | 44 | 51.8 | 2415 | 3 | US-10-104-047-730 | Sequence 730, App |
| c 6 | 44 | 51.8 | 3396 | 4 | US-10-094-749-921 | Sequence 921, App |
| c 7 | 44 | 51.8 | 421118 | 3 | US-09-949-016-16297 | Sequence 16297, A |
| c 8 | 43 | 50.6 | 170 | 3 | US-08-818-112-47 | Sequence 47, Appl |
| c 9 | 43 | 50.6 | 170 | 3 | US-08-818-111-47 | Sequence 47, Appl |
| c 10 | 43 | 50.6 | 170 | 3 | US-09-056-556-47 | Sequence 47, Appl |
| c 11 | 43 | 50.6 | 170 | 3 | US-09-072-596-47 | Sequence 47, Appl |
| c 12 | 43 | 50.6 | 170 | 3 | US-09-072-967-47 | Sequence 47, Appl |
| c 13 | 43 | 50.6 | 170 | 3 | US-10-193-002-47 | Sequence 47, Appl |
| c 14 | 43 | 50.6 | 170 | 3 | US-10-084-843-47 | Sequence 47, Appl |
| c 15 | 43 | 50.6 | 490 | 3 | US-09-401-064-317 | Sequence 317, App |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|-----------------------|-------------------|
| c 1 | 48 | 56.5 | 496 | 4 | US-09-925-065A-393797 | Sequence 393797, |
| c 2 | 48 | 56.5 | 496 | 5 | US-09-925-065A-393797 | Sequence 393797, |
| c 3 | 48 | 56.5 | 510 | 12 | US-10-301-480-461842 | Sequence 461842, |
| c 4 | 48 | 56.5 | 510 | 12 | US-10-301-480-1075251 | Sequence 1075251, |
| 5 | 48 | 56.5 | 1395 | 7 | US-10-369-493-35123 | Sequence 35123, A |
| 6 | 48 | 56.5 | 1395 | 7 | US-10-369-493-38184 | Sequence 38184, A |
| 7 | 48 | 56.5 | 1395 | 7 | US-10-369-493-38576 | Sequence 38576, A |
| 8 | 48 | 56.5 | 1407 | 7 | US-10-369-493-35741 | Sequence 35741, A |
| c 9 | 47.5 | 55.9 | 23603 | 8 | US-10-322-281-501 | Sequence 501, App |
| c 10 | 47 | 55.3 | 280 | 8 | US-10-424-599-18629 | Sequence 18629, A |
| c 11 | 47 | 55.3 | 557 | 4 | US-09-925-065A-943541 | Sequence 943541, |
| c 12 | 47 | 55.3 | 557 | 5 | US-09-925-065A-943541 | Sequence 943541, |
| c 13 | 47 | 55.3 | 588 | 12 | US-10-301-480-407966 | Sequence 407966, |
| c 14 | 47 | 55.3 | 588 | 12 | US-10-301-480-1021375 | Sequence 1021375, |
| c 15 | 47 | 55.3 | 590 | 4 | US-09-925-065A-334432 | Sequence 334432, |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|-----------------------|-------------------|
| 1 | 50 | 58.8 | 95963 | 7 | US-11-021-837-39 | Sequence 39, Appl |
| 2 | 48 | 56.5 | 564 | 8 | US-11-266-748A-100244 | Sequence 100244, |
| c 3 | 48 | 56.5 | 564 | 8 | US-11-266-748A-153055 | Sequence 153055, |
| 4 | 47 | 55.3 | 3169 | 6 | US-10-449-902-8261 | Sequence 8261, Ap |
| c 5 | 47 | 55.3 | 242825 | 8 | US-11-266-748A-32745 | Sequence 32745, A |
| 6 | 46 | 54.1 | 894 | 8 | US-11-217-529-4798 | Sequence 4798, Ap |
| 7 | 46 | 54.1 | 1000 | 8 | US-11-266-748A-200641 | Sequence 200641, |
| 8 | 46 | 54.1 | 2217 | 8 | US-11-217-529-80740 | Sequence 80740, A |
| c 9 | 45 | 52.9 | 1394 | 6 | US-10-953-349-7405 | Sequence 7405, Ap |
| 10 | 44 | 51.8 | 566 | 8 | US-11-266-748A-53448 | Sequence 53448, A |
| c 11 | 44 | 51.8 | 729 | 8 | US-11-266-748A-298624 | Sequence 298624, |
| 12 | 44 | 51.8 | 1000 | 8 | US-11-266-748A-289594 | Sequence 289594, |
| c 13 | 44 | 51.8 | 1000 | 8 | US-11-266-748A-341023 | Sequence 341023, |
| 14 | 44 | 51.8 | 1000 | 8 | US-11-266-748A-400643 | Sequence 400643, |
| c 15 | 44 | 51.8 | 1000 | 8 | US-11-266-748A-471689 | Sequence 471689, |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------|---------------------|
| 1 | 51 | 60.0 | 488 | 13 | CZ824672 | CZ824672 OC_Ba020 |
| 2 | 51 | 60.0 | 729 | 13 | CZ867792 | CZ867792 OC_Ba026 |
| 3 | 51 | 60.0 | 753 | 13 | CZ845422 | CZ845422 OC_Ba023 |
| c 4 | 51 | 60.0 | 939 | 10 | DT801726 | DT801726 126544261 |
| 5 | 50 | 58.8 | 454 | 12 | CC899139 | CC899139 ZMMBBb022 |
| c 6 | 50 | 58.8 | 597 | 14 | DX116259 | DX116259 OG_ABa014 |
| 7 | 50 | 58.8 | 699 | 12 | CC834390 | CC834390 ZMMBBb018 |
| c 8 | 50 | 58.8 | 882 | 14 | DX144504 | DX144504 OG_ABa017 |
| c 9 | 49 | 57.6 | 134 | 10 | DW587162 | DW587162 KAAK-aac4 |
| c 10 | 49 | 57.6 | 469 | 7 | BB830496 | BB830496 BB830496 |
| 11 | 49 | 57.6 | 774 | 14 | CT079213 | CT079213 Sus scrofa |
| 12 | 49 | 57.6 | 830 | 13 | DU439822 | DU439822 109842104 |
| c 13 | 49 | 57.6 | 847 | 12 | CC533118 | CC533118 CH240_410 |
| 14 | 48.5 | 57.1 | 1044 | 14 | CNS003JV | AL064902 Drosophila |
| c 15 | 48 | 56.5 | 488 | 7 | BE670147 | BE670147 7e30g10.x |

SEQ ID NO: 2

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------|--------------------|
| 1 | 60 | 100.0 | 12 | 2 | AAW15758 | Aaw15758 Peptide f |
| 2 | 60 | 100.0 | 12 | 3 | AAY87639 | Aay87639 Human bra |
| 3 | 41 | 68.3 | 879 | 8 | ADY25190 | Ady25190 Plant ful |
| 4 | 40 | 66.7 | 453 | 5 | ABB93808 | Abb93808 Herbicida |
| 5 | 40 | 66.7 | 824 | 5 | ABB93590 | Abb93590 Herbicida |
| 6 | 40 | 66.7 | 824 | 10 | AEF11437 | Aef11437 A. thalia |
| 7 | 39 | 65.0 | 123 | 7 | ADD45424 | Add45424 Human Pro |
| 8 | 39 | 65.0 | 123 | 8 | ADT66635 | Adt66635 Human Mss |
| 9 | 39 | 65.0 | 123 | 9 | ADX07140 | Adx07140 Cyclin-de |
| 10 | 39 | 65.0 | 288 | 6 | ABP57493 | Abp57493 Mycobacte |
| 11 | 39 | 65.0 | 349 | 8 | ADJ50332 | Adj50332 Oil-assoc |
| 12 | 38 | 63.3 | 1103 | 8 | ADN20575 | Adn20575 Bacterial |
| 13 | 38 | 63.3 | 2364 | 6 | ABM04816 | Abm04816 Rat micro |
| 14 | 38 | 63.3 | 2459 | 7 | ADE62725 | Ade62725 Rat Prote |
| 15 | 38 | 63.3 | 2459 | 7 | ADE62713 | Ade62713 Rat Prote |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------------------|-------------------|
| 1 | 60 | 100.0 | 12 | 2 | US-09-146-755-2 | Sequence 2, Appli |
| 2 | 60 | 100.0 | 12 | 2 | US-09-817-144-2 | Sequence 2, Appli |
| 3 | 36 | 60.0 | 169 | 2 | US-09-328-352-7861 | Sequence 7861, Ap |
| 4 | 36 | 60.0 | 402 | 2 | US-09-270-767-61053 | Sequence 61053, A |
| 5 | 36 | 60.0 | 449 | 2 | US-09-248-796A-14389 | Sequence 14389, A |
| 6 | 36 | 60.0 | 727 | 1 | US-08-424-424B-2 | Sequence 2, Appli |
| 7 | 36 | 60.0 | 727 | 3 | US-10-114-270-190 | Sequence 190, App |
| 8 | 36 | 60.0 | 727 | 5 | PCT-US94-05363A-2 | Sequence 2, Appli |
| 9 | 35.5 | 59.2 | 385 | 2 | US-09-248-796A-17673 | Sequence 17673, A |
| 10 | 35 | 58.3 | 86 | 1 | US-08-320-559-33 | Sequence 33, Appl |
| 11 | 35 | 58.3 | 86 | 2 | US-08-545-860D-33 | Sequence 33, Appl |
| 12 | 35 | 58.3 | 86 | 5 | PCT-US94-04496-33 | Sequence 33, Appl |
| 13 | 35 | 58.3 | 306 | 2 | US-09-328-352-8177 | Sequence 8177, Ap |
| 14 | 35 | 58.3 | 434 | 2 | US-08-426-630-6 | Sequence 6, Appli |
| 15 | 35 | 58.3 | 494 | 2 | US-09-006-636-8 | Sequence 8, Appli |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------------------|-------------------|
| 1 | 60 | 100.0 | 12 | 3 | US-09-817-144-2 | Sequence 2, Appli |
| 2 | 60 | 100.0 | 12 | 4 | US-10-642-587-2 | Sequence 2, Appli |
| 3 | 46 | 76.7 | 147 | 4 | US-10-437-963-192010 | Sequence 192010, |
| 4 | 41 | 68.3 | 879 | 4 | US-10-424-599-174241 | Sequence 174241, |
| 5 | 41 | 68.3 | 879 | 4 | US-10-425-114-72974 | Sequence 72974, A |
| 6 | 40 | 66.7 | 31 | 4 | US-10-424-599-244734 | Sequence 244734, |
| 7 | 39 | 65.0 | 70 | 4 | US-10-425-115-259505 | Sequence 259505, |
| 8 | 39 | 65.0 | 161 | 4 | US-10-425-115-244316 | Sequence 244316, |
| 9 | 39 | 65.0 | 181 | 4 | US-10-425-115-280076 | Sequence 280076, |
| 10 | 39 | 65.0 | 284 | 4 | US-10-767-701-40983 | Sequence 40983, A |
| 11 | 39 | 65.0 | 288 | 5 | US-10-481-265-115 | Sequence 115, App |
| 12 | 39 | 65.0 | 349 | 4 | US-10-389-566-2336 | Sequence 2336, Ap |
| 13 | 39 | 65.0 | 349 | 5 | US-10-732-923-17933 | Sequence 17933, A |
| 14 | 39 | 65.0 | 349 | 6 | US-11-188-298-13346 | Sequence 13346, A |
| 15 | 38 | 63.3 | 63 | 4 | US-10-425-115-306376 | Sequence 306376, |

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|----------------------|-------------------|
| 1 | 40 | 66.7 | 436 | 7 | US-11-056-355B-90319 | Sequence 90319, A |
| 2 | 40 | 66.7 | 436 | 7 | US-11-056-355B-94075 | Sequence 94075, A |
| 3 | 40 | 66.7 | 445 | 7 | US-11-056-355B-90318 | Sequence 90318, A |
| 4 | 40 | 66.7 | 445 | 7 | US-11-056-355B-94074 | Sequence 94074, A |
| 5 | 40 | 66.7 | 453 | 7 | US-11-056-355B-90317 | Sequence 90317, A |
| 6 | 40 | 66.7 | 453 | 7 | US-11-056-355B-94073 | Sequence 94073, A |
| 7 | 40 | 66.7 | 551 | 7 | US-11-056-355B-47130 | Sequence 47130, A |
| 8 | 40 | 66.7 | 638 | 7 | US-11-056-355B-47129 | Sequence 47129, A |
| 9 | 40 | 66.7 | 824 | 7 | US-11-056-355B-47128 | Sequence 47128, A |
| 10 | 37 | 61.7 | 258 | 6 | US-10-449-902-31034 | Sequence 31034, A |
| 11 | 37 | 61.7 | 326 | 6 | US-10-953-349-9889 | Sequence 9889, Ap |
| 12 | 37 | 61.7 | 370 | 6 | US-10-953-349-9888 | Sequence 9888, Ap |
| 13 | 37 | 61.7 | 406 | 6 | US-10-953-349-9887 | Sequence 9887, Ap |
| 14 | 37 | 61.7 | 499 | 6 | US-10-449-902-37996 | Sequence 37996, A |
| 15 | 37 | 61.7 | 825 | 6 | US-10-449-902-46177 | Sequence 46177, A |

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|--------|--------------------|
| 1 | 39 | 65.0 | 123 | 2 | I52427 | guanine-nucleotide |
| 2 | 39 | 65.0 | 288 | 2 | C70860 | hypothetical prote |
| 3 | 38 | 63.3 | 137 | 2 | S64724 | uxpB protein - Pse |
| 4 | 38 | 63.3 | 353 | 2 | S44162 | hypothetical prote |
| 5 | 38 | 63.3 | 759 | 2 | B90520 | ABC transporter at |
| 6 | 38 | 63.3 | 881 | 2 | T25786 | hypothetical prote |
| 7 | 38 | 63.3 | 2364 | 2 | A56577 | microtubule-associ |
| 8 | 37 | 61.7 | 212 | 2 | AG1050 | conserved hypothet |
| 9 | 37 | 61.7 | 290 | 2 | S59322 | hypothetical prote |
| 10 | 37 | 61.7 | 359 | 2 | S46714 | hypothetical prote |
| 11 | 37 | 61.7 | 402 | 2 | AH0896 | propionate kinase |
| 12 | 37 | 61.7 | 484 | 2 | G86362 | beta-glucanase [im |
| 13 | 37 | 61.7 | 504 | 2 | T01603 | hypothetical prote |
| 14 | 37 | 61.7 | 772 | 2 | B65167 | hypothetical 88.1 |
| 15 | 36 | 60.0 | 146 | 2 | C97130 | probable 4-Cys fer |

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|---------------|--------------------|
| 1 | 47 | 78.3 | 271 | 2 | Q386N0_9TRYP | Q386n0 trypanosoma |
| 2 | 45 | 75.0 | 745 | 2 | Q4ING0_GIBZE | Q4ing0 gibberella |
| 3 | 43 | 71.7 | 655 | 2 | Q6P3A3_MOUSE | Q6p3a3 mus musculu |
| 4 | 43 | 71.7 | 1231 | 2 | Q3UE14_MOUSE | Q3ue14 mus musculu |
| 5 | 43 | 71.7 | 1348 | 2 | Q70X02_MOUSE | Q70x02 mus musculu |
| 6 | 43 | 71.7 | 1349 | 2 | Q7TNB8_MOUSE | Q7tnb8 mus musculu |
| 7 | 42 | 70.0 | 416 | 2 | Q4XP04_PLACH | Q4xp04 plasmodium |
| 8 | 42 | 70.0 | 878 | 2 | Q6FRP4_CANGA | Q6frp4 candida gla |
| 9 | 41 | 68.3 | 175 | 2 | Q815Y1_BACCR | Q815y1 bacillus ce |
| 10 | 41 | 68.3 | 175 | 2 | Q72Y89_BACCC1 | Q72y89 bacillus ce |
| 11 | 41 | 68.3 | 380 | 2 | Q2J7J8_9ACTO | Q2j7j8 frankia sp. |
| 12 | 41 | 68.3 | 652 | 2 | Q5B9B7_EMENI | Q5b9b7 aspergillus |
| 13 | 41 | 68.3 | 1131 | 2 | Q72WT6_DESVH | Q72wt6 desulfovibr |
| 14 | 40 | 66.7 | 254 | 2 | Q6U478_9HEPC | Q6u478 hepatitis c |
| 15 | 40 | 66.7 | 254 | 2 | Q6U479_9HEPC | Q6u479 hepatitis c |

NA ENCODING SEQ ID NO: 2

SUMMARIES

| | | % Query | | | | | |
|------------|-------|---------|--------|--------|----|--------------|--------------------|
| Result No. | Score | Match | Length | DB | ID | Description | |
| c | 1 | 50 | 83.3 | 79534 | 11 | CR628324 | CR628324 Zebrafish |
| c | 2 | 47 | 78.3 | 173849 | 5 | AC078855 | AC078855 Homo sapi |
| | 3 | 47 | 78.3 | 201708 | 12 | AC020731 | AC020731 Homo sapi |
| c | 4 | 46 | 76.7 | 110000 | 4 | AP008210_020 | Continuation (21 o |
| c | 5 | 46 | 76.7 | 126447 | 4 | OSJN00189 | AL662985 Oryza sat |
| c | 6 | 45 | 75.0 | 110000 | 12 | AC110933_2 | Continuation (3 of |
| c | 7 | 45 | 75.0 | 196855 | 12 | AC022297 | AC022297 Mus muscu |
| c | 8 | 45 | 75.0 | 197046 | 5 | AC009123 | AC009123 Homo sapi |
| | 9 | 45 | 75.0 | 200006 | 12 | AC166338 | AC166338 Mus muscu |
| | 10 | 45 | 75.0 | 204037 | 6 | AL596207 | AL596207 Mouse DNA |
| | 11 | 45 | 75.0 | 210246 | 11 | BX511081 | BX511081 Zebrafish |
| | 12 | 45 | 75.0 | 216522 | 12 | AC139664 | AC139664 Homo sapi |
| | 13 | 45 | 75.0 | 238816 | 12 | AC108616 | AC108616 Rattus no |
| | 14 | 45 | 75.0 | 252612 | 12 | AC111263 | AC111263 Rattus no |
| c | 15 | 44 | 73.3 | 3340 | 4 | AK119411 | AK119411 Oryza sat |

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description | |
|------------|-------|---------|--------|--------|----|-------------|--------------------|
| | | Match | Length | | | | |
| c | 1 | 46 | 76.7 | 351 | 12 | ADJ39880 | Adj39880 Plant cDN |
| c | 2 | 44 | 73.3 | 1578 | 11 | ACL28106 | Acl28106 Rice abio |
| c | 3 | 44 | 73.3 | 26995 | 5 | AAS29963 | Aas29963 Human lun |
| c | 4 | 44 | 73.3 | 26995 | 10 | ADB33300 | Adb33300 Human nov |
| c | 5 | 43 | 71.7 | 213 | 8 | ABX48104 | Abx48104 Bovine ES |
| c | 6 | 43 | 71.7 | 408 | 8 | ABX43534 | Abx43534 Bovine ES |
| c | 7 | 43 | 71.7 | 185548 | 13 | ADV34986 | Adv34986 Murine cD |
| | 8 | 41 | 68.3 | 3049 | 13 | ADX32390 | Adx32390 Plant ful |
| | 9 | 40 | 66.7 | 933 | 13 | ADX33233 | Adx33233 Plant ful |
| | 10 | 40 | 66.7 | 1362 | 14 | ADW07578 | Adw07578 GTase cDN |
| | 11 | 40 | 66.7 | 1810 | 13 | ADX31096 | Adx31096 Plant ful |
| | 12 | 40 | 66.7 | 1841 | 12 | ADO62400 | Ado62400 Transcrip |
| | 13 | 40 | 66.7 | 2821 | 15 | AEF11436 | Aef11436 A. thalia |
| | 14 | 40 | 66.7 | 48995 | 9 | ADA02579 | Ada02579 Mouse Rel |
| | 15 | 40 | 66.7 | 48995 | 10 | ADB72317 | Adb72317 Mouse Rel |

SUMMARIES

| | | Query | | | | | | |
|------------|-------|-------|--------|-----|----|----------------------|-------------------|--|
| Result No. | Score | Match | Length | DB | ID | Description | | |
| c | 1 | 39 | 65.0 | 275 | 3 | US-09-513-999C-11209 | Sequence 11209, A | |
| | 2 | 39 | 65.0 | 459 | 3 | US-09-020-956-142 | Sequence 142, App | |
| | 3 | 39 | 65.0 | 459 | 3 | US-09-030-607-142 | Sequence 142, App | |
| | 4 | 39 | 65.0 | 459 | 3 | US-09-439-313-142 | Sequence 142, App | |
| | 5 | 39 | 65.0 | 459 | 3 | US-09-352-616A-142 | Sequence 142, App | |
| | 6 | 39 | 65.0 | 459 | 3 | US-09-232-149A-142 | Sequence 142, App | |
| | 7 | 39 | 65.0 | 459 | 3 | US-09-159-812-142 | Sequence 142, App | |
| | 8 | 39 | 65.0 | 459 | 3 | US-09-636-215-142 | Sequence 142, App | |
| | 9 | 39 | 65.0 | 459 | 3 | US-09-685-166A-142 | Sequence 142, App | |
| | 10 | 39 | 65.0 | 459 | 3 | US-09-115-453-142 | Sequence 142, App | |
| | 11 | 39 | 65.0 | 459 | 3 | US-09-688-489-142 | Sequence 142, App | |
| | 12 | 39 | 65.0 | 459 | 3 | US-09-679-426-142 | Sequence 142, App | |
| | 13 | 39 | 65.0 | 459 | 3 | US-09-759-143-142 | Sequence 142, App | |
| | 14 | 39 | 65.0 | 459 | 3 | US-09-651-236-142 | Sequence 142, App | |
| | 15 | 39 | 65.0 | 459 | 3 | US-09-030-606-142 | Sequence 142, App | |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|-----------------------|-------------------|
| c 1 | 46 | 76.7 | 351 | 8 | US-10-260-238-880 | Sequence 880, App |
| c 2 | 46 | 76.7 | 649 | 8 | US-10-437-963-89527 | Sequence 89527, A |
| 3 | 45 | 75.0 | 740 | 6 | US-10-027-632-21907 | Sequence 21907, A |
| 4 | 45 | 75.0 | 740 | 6 | US-10-027-632-148770 | Sequence 148770, |
| 5 | 45 | 75.0 | 740 | 6 | US-10-027-632-148771 | Sequence 148771, |
| 6 | 45 | 75.0 | 740 | 7 | US-10-027-632-21907 | Sequence 21907, A |
| 7 | 45 | 75.0 | 740 | 7 | US-10-027-632-148770 | Sequence 148770, |
| 8 | 45 | 75.0 | 740 | 7 | US-10-027-632-148771 | Sequence 148771, |
| c 9 | 45 | 75.0 | 996 | 12 | US-10-301-480-542262 | Sequence 542262, |
| c 10 | 45 | 75.0 | 996 | 12 | US-10-301-480-1155671 | Sequence 1155671, |
| c 11 | 44 | 73.3 | 26995 | 3 | US-09-764-878-227 | Sequence 227, App |
| c 12 | 44 | 73.3 | 26995 | 6 | US-10-079-854-227 | Sequence 227, App |
| c 13 | 43 | 71.7 | 213 | 3 | US-09-960-352-13269 | Sequence 13269, A |
| c 14 | 43 | 71.7 | 408 | 3 | US-09-960-352-8699 | Sequence 8699, Ap |
| c 15 | 43 | 71.7 | 185548 | 6 | US-10-175-523-62 | Sequence 62, Appl |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|-----------------------|-------------------|
| 1 | 41 | 68.3 | 3065 | 8 | US-11-216-545-7473 | Sequence 7473, Ap |
| 2 | 40 | 66.7 | 1362 | 7 | US-11-056-355B-90316 | Sequence 90316, A |
| 3 | 40 | 66.7 | 1362 | 7 | US-11-056-355B-94072 | Sequence 94072, A |
| 4 | 40 | 66.7 | 1617 | 6 | US-10-953-349-34007 | Sequence 34007, A |
| 5 | 40 | 66.7 | 1617 | 7 | US-11-056-355B-12275 | Sequence 12275, A |
| 6 | 40 | 66.7 | 1617 | 7 | US-11-056-355B-19622 | Sequence 19622, A |
| 7 | 40 | 66.7 | 1840 | 7 | US-11-218-305-1839 | Sequence 1839, Ap |
| 8 | 40 | 66.7 | 2704 | 7 | US-11-056-355B-47127 | Sequence 47127, A |
| c 9 | 39 | 65.0 | 420 | 8 | US-11-266-748A-170341 | Sequence 170341, |
| 10 | 39 | 65.0 | 420 | 8 | US-11-266-748A-245047 | Sequence 245047, |
| c 11 | 39 | 65.0 | 804 | 8 | US-11-217-529-5397 | Sequence 5397, Ap |
| c 12 | 39 | 65.0 | 952 | 8 | US-11-266-748A-228170 | Sequence 228170, |
| 13 | 39 | 65.0 | 1000 | 8 | US-11-266-748A-216407 | Sequence 216407, |
| c 14 | 39 | 65.0 | 1000 | 8 | US-11-266-748A-287356 | Sequence 287356, |
| 15 | 39 | 65.0 | 1000 | 8 | US-11-266-748A-338785 | Sequence 338785, |

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------|--------------------|
| c 1 | 48 | 80.0 | 500 | 14 | DX113407 | DX113407 OG_ABa013 |
| c 2 | 48 | 80.0 | 663 | 14 | DX118759 | DX118759 OG_ABa014 |
| c 3 | 48 | 80.0 | 695 | 14 | DX129614 | DX129614 OG_ABa015 |
| 4 | 48 | 80.0 | 714 | 14 | DX124014 | DX124014 OG_ABa015 |
| c 5 | 48 | 80.0 | 717 | 13 | DU159234 | DU159234 OG_ABa004 |
| c 6 | 48 | 80.0 | 732 | 14 | DX135548 | DX135548 OG_ABa016 |
| 7 | 48 | 80.0 | 741 | 14 | DU809699 | DU809699 OG_ABa010 |
| c 8 | 48 | 80.0 | 754 | 14 | DX153357 | DX153357 OG_ABa019 |
| c 9 | 48 | 80.0 | 766 | 14 | DU663919 | DU663919 OG_ABa007 |
| c 10 | 48 | 80.0 | 767 | 14 | DU634863 | DU634863 OO_Ba014 |
| 11 | 48 | 80.0 | 820 | 13 | DU161578 | DU161578 OG_ABa004 |
| c 12 | 47 | 78.3 | 616 | 11 | AQ652025 | AQ652025 Sheared D |
| c 13 | 46 | 76.7 | 351 | 13 | CL967949 | CL967949 OsIFCC016 |
| c 14 | 46 | 76.7 | 427 | 1 | AI001826 | AI001826 ov22g11.s |
| 15 | 46 | 76.7 | 561 | 5 | CD424221 | CD424221 SA1_4_B02 |

10/642,587

Sequence alignment A

SEQ ID NO: 1

QQBEG6

HWLF1 protein - human cytomegalovirus (strain AD169)

N;Alternate names: hypothetical protein US22

C;Species: human cytomegalovirus, human herpesvirus 5

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C;Accession: F27231; S09936

R;Weston, K.; Barrell, B.G.

J. Mol. Biol. 192, 177-208, 1986

A;Title: Sequence of the short unique region, short repeats, and part of the long repeats of human cytomegalovirus.

A;Reference number: A92935; MUID:87169717; PMID:3031311

A;Accession: F27231

A;Molecule type: DNA

A;Residues: 1-593 <WES>

A;Cross-references: UNIPROT:P09722; UNIPARC:UPI0000137E39; EMBL:X04650; NID:g59801;

PIDN:CAB37114.1; PID:g4456195

A;Experimental source: strain AD169

R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;

Hutchison III, C.A.; Kouzarides, T.; Martignetti, J.A.; Preddie, E.; Satchwell, S.C.;

Tomlinson, P.; Weston, K.M.; Barrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.

A;Reference number: S09749; MUID:90269039; PMID:2161319

A;Accession: S09936

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-593 <CHE>

A;Cross-references: UNIPARC:UPI0000137E39; EMBL:X17403; NID:g59591; PIDN:CAA35289.1;

PID:gl780953

A;Experimental source: strain AD169

A;Note: this sequence was submitted to the EMBL Data Library, December 1989

A;Note: this reading frame extends between two stop codons and does not begin with a start codon

C;Genetics:

A;Gene: HWLF1

C;Superfamily: cytomegalovirus HHLF5 protein

Query Match 47.1%; Score 40; DB 1; Length 593;

Best Local Similarity 57.1%; Pred. No. 68;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KAGVAFLHKNDID 15

| | | : | | | |

Db 314 KFGVVYLHKIEDSD 327

10/642,587
Sequence alignment B
SEQ ID NO: 2
A32183
tropomyosin TPM1 - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein N2332; protein YNL079c
C;Species: *Saccharomyces cerevisiae*
C;Date: 08-Sep-1989 #sequence_revision 08-Sep-1989 #text_change 31-Dec-2004
C;Accession: A32183; S53899; S63011; S63018; S63928
R;Liu, H.; Bretscher, A.
Cell 57, 233-242, 1989
A;Title: Disruption of the single tropomyosin gene in yeast results in the disappearance of actin cables from the cytoskeleton.
A;Reference number: A32183; MUID:89195234; PMID:2649250
A;Accession: A32183
A;Molecule type: DNA
A;Residues: 1-199 <LIU>
A;Cross-references: UNIPROT:P17536; UNIPARC:UPI0000137254; EMBL:M25501; NID:g173037; PIDN:AAA35174.1; PID:g173038
R;Poehlmann, R.; Philippsen, P.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53896
A;Accession: S53899
A;Molecule type: DNA
A;Residues: 1-199 <POE>
A;Cross-references: UNIPARC:UPI0000137254; EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
R;Poehlmann, R.; Philippsen, P.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62997
A;Accession: S63011
A;Molecule type: DNA
A;Residues: 1-199 <POW>
A;Cross-references: UNIPARC:UPI0000137254; EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL079c
A;Experimental source: strain S288C
R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63018
A;Accession: S63018
A;Molecule type: DNA
A;Residues: 1-199 <SOL>
A;Cross-references: UNIPARC:UPI0000137254; EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL079c
A;Experimental source: strain S288C
R;Poehlmann, R.; Philippsen, P.
Yeast 12, 391-402, 1996
A;Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12 new open reading frames (ORFs) and an ancient duplication of six ORFs.
A;Reference number: S63925; MUID:96267764; PMID:8701611
A;Accession: S63928
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-199 <POF>
A;Cross-references: UNIPARC:UPI0000137254; EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C;Genetics:
A;Gene: SGD:TPM1
A;Cross-references: SGD:S0005023; MIPS:YNL079c
A;Map position: 14L
C;Superfamily: slime mold ribozyme I
C;Keywords: coiled coil; cytoskeleton

Query Match 60.0%; Score 36; DB 2; Length 199;
Best Local Similarity 63.6%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GLSDGSNTESD 11
||| |
Db 63 GLSDSKQTEQD 73